

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/874,198

CRF Processing Date: 3/11/2002
 Edited by: A
 Verified by: A (STIC staff)

ENTERED

OIPE 03/10
 # 3

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 1 - corrected amino acid numbering



OIPE

RAW SEQUENCE LISTING

DATE: 03/11/2002

PATENT APPLICATION: US/09/874,198

TIME: 18:09:09

Input Set : N:\Crf3\02262002\I874198.raw

Output Set: N:\CRF3\03112002\I874198.raw

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1 <110> APPLICANT: Jensenius, Jens Chr.
2   Thiel, Steffen
3 <120> TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND
4   USES FOR IT
5 <130> FILE REFERENCE: 09011-002002
6 <140> CURRENT APPLICATION NUMBER: US/09/874,198
7 <141> CURRENT FILING DATE: 2001-06-04
8 <150> PRIOR APPLICATION NUMBER: 09/054,218
9 <151> PRIOR FILING DATE: 1998-04-02
10 <150> PRIOR APPLICATION NUMBER: 60/042,678
11 <151> PRIOR FILING DATE: 1997-04-03
12 <160> NUMBER OF SEQ ID NOS: 8
13 <170> SOFTWARE: FastSEQ for Windows Version 4.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 41
17 <212> TYPE: PRT
18 <213> ORGANISM: Homo sapiens
19 <400> SEQUENCE: 1
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21       1           5           10           15
22   Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
23           20           25           30
24   Thr Leu Thr Ala Pro Pro Gly Tyr Arg
25       35           40
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 686
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
31 <400> SEQUENCE: 2
32   Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
33       1           5           10           15
34   Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
35           20           25           30
36   Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
37       35           40           45
38   Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
39       50           55           60
40   Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
41       65           70           75           80
42   Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
43           85           90           95
44   Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
45       100          105          110

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46   Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
47           115                      120                      125
48   Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
49           130                      135                      140
50   Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
51           145                      150                      155                      160
52   Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
53           165                      170                      175
54   Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
55           180                      185                      190
56   Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
57           195                      200                      205
58   Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
59           210                      215                      220
60   Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
61           225                      230                      235                      240
62   Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
63           245                      250                      255
64   Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
65           260                      265                      270
66   Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
67           275                      280                      285
68   Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
69           290                      295                      300
70   Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
71           305                      310                      315                      320
72   Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
73           325                      330                      335
74   Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
75           340                      345                      350
76   Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly Pro
77           355                      360                      365
78   Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
79           370                      375                      380
80   Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
81           385                      390                      395                      400
82   Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly
83           405                      410                      415
84   Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu Pro
85           420                      425                      430
86   Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly Gly
87           435                      440                      445
88   Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu Gly
89           450                      455                      460
90   Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
91           465                      470                      475                      480
92   Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
93           485                      490                      495
94   Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala

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95		500		505		510													
96	Trp	Ser	Glu	Ala	Val	Phe	Ile	His	Glu	Gly	Tyr	Thr	His	Asp	Ala	Gly			
97			515					520					525						
98	Phe	Asp	Asn	Asp	Ile	Ala	Leu	Ile	Lys	Leu	Asn	Asn	Lys	Val	Val	Ile			
99		530					535					540							
100	Asn	Ser	Asn	Ile	Thr	Pro	Ile	Cys	Leu	Pro	Arg	Lys	Glu	Ala	Glu	Ser			
101		545				550					555					560			
102	Phe	Met	Arg	Thr	Asp	Asp	Ile	Gly	Thr	Ala	Ser	Gly	Trp	Gly	Leu	Thr			
103				565						570					575				
104	Gln	Arg	Gly	Phe	Leu	Ala	Arg	Asn	Leu	Met	Tyr	Val	Asp	Ile	Pro	Ile			
105			580					585					590						
106	Val	Asp	His	Gln	Lys	Cys	Thr	Ala	Ala	Tyr	Glu	Lys	Pro	Pro	Tyr	Pro			
107			595					600					605						
108	Arg	Gly	Ser	Val	Thr	Ala	Asn	Met	Leu	Cys	Ala	Gly	Leu	Glu	Ser	Gly			
109		610					615					620							
110	Gly	Lys	Asp	Ser	Cys	Arg	Gly	Asp	Ser	Gly	Gly	Ala	Leu	Val	Phe	Leu			
111		625				630					635				640				
112	Asp	Ser	Glu	Thr	Glu	Arg	Trp	Phe	Val	Gly	Gly	Ile	Val	Ser	Trp	Gly			
113				645						650					655				
114	Ser	Met	Asn	Cys	Gly	Glu	Ala	Gly	Gln	Tyr	Gly	Val	Tyr	Thr	Lys	Val			
115			660					665					670						
116	Ile	Asn	Tyr	Ile	Pro	Trp	Ile	Glu	Asn	Ile	Ile	Ser	Asp	Phe					
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120	<211>	LENGTH:	2475																
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123	<220>	FEATURE:																	
124	<221>	NAME/KEY:	CDS																
125	<222>	LOCATION:	(37)...(2094)																
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128					Met	Arg	Leu	Leu	Thr	Leu									
129					1				5										
130	ctg	ggc	ctt	ctg	tgt	ggc	tcg	gtg	gcc	acc	ccc	tta	ggc	ccg	aag	tgg			102
131	Leu	Gly	Leu	Leu	Cys	Gly	Ser	Val	Ala	Thr	Pro	Leu	Gly	Pro	Lys	Trp			
132			10					15					20						
133	cct	gaa	cct	gtg	ttc	ggg	cgc	ctg	gca	tcc	ccc	ggc	ttt	cca	ggg	gag			150
134	Pro	Glu	Pro	Val	Phe	Gly	Arg	Leu	Ala	Ser	Pro	Gly	Phe	Pro	Gly	Glu			
135		25					30					35							
136	tat	gcc	aat	gac	cag	gag	cgg	cgc	tgg	acc	ctg	act	gca	ccc	ccc	ggc			198
137	Tyr	Ala	Asn	Asp	Gln	Glu	Arg	Arg	Trp	Thr	Leu	Thr	Ala	Pro	Pro	Gly			
138		40				45					50								
139	tac	cgc	ctg	cgc	ctc	tac	ttc	acc	cac	ttc	gac	ctg	gag	ctc	tcc	cac			246
140	Tyr	Arg	Leu	Arg	Leu	Tyr	Phe	Thr	His	Phe	Asp	Leu	Glu	Leu	Ser	His			
141		55				60				65					70				
142	ctc	tgc	gag	tac	gac	ttc	gtc	aag	ctg	agc	tcg	ggg	gcc	aag	gtg	ctg			294
143	Leu	Cys	Glu	Tyr	Asp	Phe	Val	Lys	Leu	Ser	Ser	Gly	Ala	Lys	Val	Leu			
144					75				80						85				

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145	gcc acg ctg tgc ggg cag gag agc aca gac acg gag cgg gcc cct ggc	342
146	Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly	
147	90 95 100	
148	aag gac act ttc tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc	390
149	Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg	
150	105 110 115	
151	tcc gac tac tcc aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat	438
152	Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr	
153	120 125 130	
154	gca gcc gag gac att gac gag tgc cag gtg gcc ccg gga gag gcg ccc	486
155	Ala Ala Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro	
156	135 140 145 150	
157	acc tgc gac cac cac tgc cac aac cac ctg ggc ggt ttc tac tgc tcc	534
158	Thr Cys Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser	
159	155 160 165	
160	tgc cgc gca ggc tac gtc ctg cac cgt aac aag cgc acc tgc tca gcc	582
161	Cys Arg Ala Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Ala	
162	170 175 180	
163	ctg tgc tcc ggc cag gtc ttc acc cag agg tct ggg gag ctc agc agc	630
164	Leu Cys Ser Gly Gln Val Phe Thr Gln Arg Ser Gly Glu Leu Ser Ser	
165	185 190 195	
166	cct gaa tac cca cgg ccg tat ccc aaa ctc tcc agt tgc act tac agc	678
167	Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser	
168	200 205 210	
169	atc agc ctg gag gag ggg ttc agt gtc att ctg gac ttt gtg gag tcc	726
170	Ile Ser Leu Glu Glu Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser	
171	215 220 225 230	
172	ttc gat gtg gag aca cac cct gaa acc ctg tgt ccc tac gac ttt ctc	774
173	Phe Asp Val Glu Thr His Pro Glu Thr Leu Cys Pro Tyr Asp Phe Leu	
174	235 240 245	
175	aag att caa aca gac aga gaa gaa cat ggc cca ttc tgt ggg aag aca	822
176	Lys Ile Gln Thr Asp Arg Glu Glu His Gly Pro Phe Cys Gly Lys Thr	
177	250 255 260	
178	ttg ccc cac agg att gaa aca aaa agc aac acg gtg acc atc acc ttt	870
179	Leu Pro His Arg Ile Glu Thr Lys Ser Asn Thr Val Thr Ile Thr Phe	
180	265 270 275	
181	gtc aca gat gaa tca gga gac cac aca ggc tgg aag atc cac tac acg	918
182	Val Thr Asp Glu Ser Gly Asp His Thr Gly Trp Lys Ile His Tyr Thr	
183	280 285 290	
184	agc aca gcg cag cct tgc cct tat ccg atg gcg cca cct aat ggc cac	966
185	Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met Ala Pro Pro Asn Gly His	
186	295 300 305 310	
187	gtt tca cct gtg caa gcc aaa tac atc ctg aaa gac agc ttc tcc atc	1014
188	Val Ser Pro Val Gln Ala Lys Tyr Ile Leu Lys Asp Ser Phe Ser Ile	
189	315 320 325	
190	ttt tgc gag act ggc tat gag ctt ctg caa ggt cac ttg ccc ctg aaa	1062
191	Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln Gly His Leu Pro Leu Lys	
192	330 335 340	
193	tcc ttt act gca gtt tgt cag aaa gat gga tct tgg gac cgg cca atg	1110

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194	Ser	Phe	Thr	Ala	Val	Cys	Gln	Lys	Asp	Gly	Ser	Trp	Asp	Arg	Pro	Met	
195			345					350					355				
196	ccc	gcg	tgc	agc	att	gtt	gac	tgt	ggc	cct	cct	gat	gat	cta	ccc	agt	1158
197	Pro	Ala	Cys	Ser	Ile	Val	Asp	Cys	Gly	Pro	Pro	Asp	Asp	Leu	Pro	Ser	
198			360				365					370					
199	ggc	cga	gtg	gag	tac	atc	aca	ggc	cct	gga	gtg	acc	tac	aaa	gct		1206
200	Gly	Arg	Val	Glu	Tyr	Ile	Thr	Gly	Pro	Gly	Val	Thr	Thr	Tyr	Lys	Ala	
201	375					380					385				390		
202	gtg	att	cag	tac	agc	tgt	gaa	gag	acc	ttc	tac	aca	atg	aaa	gtg	aat	1254
203	Val	Ile	Gln	Tyr	Ser	Cys	Glu	Glu	Thr	Phe	Tyr	Thr	Met	Lys	Val	Asn	
204					395					400					405		
205	gat	ggc	aaa	tat	gtg	tgt	gag	gct	gat	gga	ttc	tgg	acg	agc	tcc	aaa	1302
206	Asp	Gly	Lys	Tyr	Val	Cys	Glu	Ala	Asp	Gly	Phe	Trp	Thr	Ser	Ser	Lys	
207				410					415					420			
208	gga	gaa	aaa	tca	ctc	cca	gtc	tgt	gag	cct	gtt	tgt	gga	cta	tca	gcc	1350
209	Gly	Glu	Lys	Ser	Leu	Pro	Val	Cys	Glu	Pro	Val	Cys	Gly	Leu	Ser	Ala	
210			425					430					435				
211	cgc	aca	aca	gga	ggg	cgt	ata	tat	gga	ggg	caa	aag	gca	aaa	cct	ggc	1398
212	Arg	Thr	Thr	Gly	Gly	Arg	Ile	Tyr	Gly	Gly	Gln	Lys	Ala	Lys	Pro	Gly	
213			440				445					450					
214	gat	ttt	cct	tgg	caa	gtc	ctg	ata	tta	ggc	gga	acc	aca	gca	gca	ggc	1446
215	Asp	Phe	Pro	Trp	Gln	Val	Leu	Ile	Leu	Gly	Gly	Thr	Thr	Ala	Ala	Gly	
216	455					460				465						470	
217	gca	ctt	tta	tat	gac	aac	tgg	gtc	cta	aca	gct	gct	cat	gcc	gtc	tat	1494
218	Ala	Leu	Leu	Tyr	Asp	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Ala	Val	Tyr	
219					475					480					485		
220	gag	caa	aaa	cat	gat	gca	tcc	gcc	ctg	gac	att	cga	atg	ggc	acc	ctg	1542
221	Glu	Gln	Lys	His	Asp	Ala	Ser	Ala	Leu	Asp	Ile	Arg	Met	Gly	Thr	Leu	
222				490					495					500			
223	aaa	aga	cta	tca	cct	cat	tat	aca	caa	gcc	tgg	tct	gaa	gct	gtt	ttt	1590
224	Lys	Arg	Leu	Ser	Pro	His	Tyr	Thr	Gln	Ala	Trp	Ser	Glu	Ala	Val	Phe	
225				505				510					515				
226	ata	cat	gaa	ggc	tat	act	cat	gat	gct	ggc	ttt	gac	aat	gac	ata	gca	1638
227	Ile	His	Glu	Gly	Tyr	Thr	His	Asp	Ala	Gly	Phe	Asp	Asn	Asp	Ile	Ala	
228			520				525					530					
229	ctg	att	aaa	ttg	aat	aac	aaa	gtt	gta	atc	aat	agc	aac	atc	acg	cct	1686
230	Leu	Ile	Lys	Leu	Asn	Asn	Lys	Val	Val	Ile	Asn	Ser	Asn	Ile	Thr	Pro	
231	535					540					545					550	
232	att	tgt	ctg	cca	aga	aaa	gaa	gct	gaa	tcc	ttt	atg	agg	aca	gat	gac	1734
233	Ile	Cys	Leu	Pro	Arg	Lys	Glu	Ala	Glu	Ser	Phe	Met	Arg	Thr	Asp	Asp	
234					555					560					565		
235	att	gga	act	gca	tct	gga	tgg	gga	tta	acc	caa	agg	ggc	ttt	ctt	gct	1782
236	Ile	Gly	Thr	Ala	Ser	Gly	Trp	Gly	Leu	Thr	Gln	Arg	Gly	Phe	Leu	Ala	
237				570					575					580			
238	aga	aat	cta	atg	tat	gtc	gac	ata	ccg	att	gtt	gac	cat	caa	aaa	tgt	1830
239	Arg	Asn	Leu	Met	Tyr	Val	Asp	Ile	Pro	Ile	Val	Asp	His	Gln	Lys	Cys	
240			585					590					595				
241	act	gct	gca	tat	gaa	aag	cca	ccc	tat	cca	agg	gga	agt	gta	act	gct	1878
242	Thr	Ala	Ala	Tyr	Glu	Lys	Pro	Pro	Tyr	Pro	Arg	Gly	Ser	Val	Thr	Ala	

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